

In the Claims:

Please cancel claims 6, 9 and 37 without prejudice and amend the claims as follows:

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1. (currently amended) A method of ~~performing real time infection control tracking spread of infectious bacteria~~, comprising:  
obtaining a sample of a ~~microorganism~~ bacterium;  
sequencing a first region of a ~~deoxyribonucleic acid~~ from the ~~microorganism~~ bacterium sample, ~~the first region comprising a plurality of repeating sequences of nucleotides~~;  
comparing the first sequenced region with historical sequence data ~~derived from known bacteria of the same species and stored in a database~~;  
determining a measure of phylogenetic relatedness between the first sequenced region of the ~~microorganism~~ bacterium sample and the historical sequence data stored in the database based upon differences between the first sequenced region of the ~~microorganism~~ bacterium sample and the historical sequence data;  
~~identifying patients infected or objects contaminated with the bacterium providing infection control information based on the phylogenetic relatedness determination; and tracking the spread of the bacteria utilizing the identified infected patients and contaminated objects infection control information in the real time control or prevention of the spread of an infection.~~

2. canceled

3. (currently amended) The method of claim 1, wherein the database is a centralized database located ~~in an infection control facility, remote from where the sample is obtained the infection control facility transmitting infection control information to the remote facility via a computer network.~~

4. (currently amended) The method of claim 1, wherein the database is located in the same location as where the ~~microorganism~~ sample is obtained.

5. (currently amended) The method of claim 1, wherein the first region that is sequenced is a region having a mutation rate ~~which is suitably fast for performing real time infection control sufficient to differentiate between subspecies to determine phylogenetic relatedness and to track the bacteria.~~

6. canceled

7. (currently amended) The method of claim 6, wherein the ~~microorganism bacterium~~ is *Staphylococcus aureus* and the first region is located in the protein A gene or the coagulase gene.

8. (currently amended) The method of claim 7, wherein the ~~microorganism bacterium~~ sample is obtained from a ~~prospective patient before as the patient is admitted to a health care facility and prior to being exposed to patients in a the health care facility.~~

9. canceled

10. (currently amended) The method of claim 1, further including:

obtaining a medical history from a patient from which the ~~microorganism~~ bacterium sample was taken;

determining an infection risk factor based on the patient's medical history, the infection risk factor being a measure of the patient's risk of acquiring an infection; and taking appropriate infection control measures in accordance with the infection risk factor.

11. (currently amended) The method of claim 10, further including:

transmitting the patient's medical history to the database without transmitting ~~sensitive private~~ patient information; and

storing the ~~sensitive private~~ patient information in a local database at the remote from the database that the patient's medical history is transmitted to.

12. (currently amended) The method of claim 1, wherein the step of sequencing comprises either:

a) sequencing the ~~microorganism sample~~ first region at a remote facility and transmitting the resulting sequence data to the database via a computer network; or

b) sending the ~~microorganism bacterium~~ sample to an infection control facility associated with the database, sequencing the ~~microorganism~~ first region at the infection control facility, and storing the sequence data in the database.

13. (original) The method of claim 1, wherein the first region is identified by a set of

primers.

14. (original) The method of claim 1, wherein the first region is amplified prior to sequencing.

15. (currently amended) The method of claim 1, wherein the step of determining the phylogenetic relatedness between the ~~microorganism sample~~ first region and a historical sample represented by the historical sequence data stored in the database includes one of the following:

- a) calculating a relative cost between the ~~two samples~~ first region and the historical sample; or
- b) calculating an absolute cost for ~~each sample~~ the bacterium sample and the known bacteria and comparing the absolute costs.

16. (currently amended) The method of claim 1, wherein the step of determining the phylogenetic relatedness between the ~~microorganism sample~~ first region and a historical sample represented by the historical sequence data stored in the database includes:

identifying repeat sequences in the sequenced first region ~~of the microorganism sample~~ and the historical samples sample; and

comparing a similarity between a repeat motif in the ~~microorganism sample~~ sequence of the first region and a repeat motif in a corresponding ~~historical sample~~ sequence in the historical sample; and

determining a repeat motif cost that is a measure of phylogenetic relatedness between the samples based on the similarity between the repeat motifs.

17. (currently amended) The method of claim 16, further including:

comparing a similarity between individual base-pair sequence in the ~~microorganism sample~~ first region and the individual base-pair sequence in the corresponding historical sample;  
and

determining a point mutation cost that is measure of phylogenetic relatedness between the samples based on the similarity between the individual base pair sequences.

18. (original) The method of claim 17, further including:

determining a total cost based on a weighted combination of the repeat motif cost and the point mutation cost.

19. (currently amended) The method of claim 16, further including:

calculating a phylogenetic relatedness between the first region sample and a the historical sample, wherein the deletion or insertion of a repeat sequence is treated as a single event.

20. (original) The method of claim 19, wherein a point mutation is treated as a single event.

21. (currently amended) The method of claim 1, wherein the step of determining the phylogenetic relatedness between the first sequenced region ~~of the microorganism sample~~ and the historical sequence data stored in the database includes at least one of:

comparing the first sequenced region ~~of the microorganism sample~~ to historical sequence

data representing samples obtained from the same location as the ~~microorganism sample first region~~, thereby determining a local phylogenetic relatedness;

comparing the first sequenced region of ~~the microorganism sample~~ to historical sequence data representing samples obtained from the same geographical region as where the ~~microorganism bacterium~~ sample was taken, thereby determining a regional phylogenetic relatedness; and

comparing the first sequenced region of ~~the microorganism sample~~ to historical sequence data representing global historical samples, thereby determining a global phylogenetic relatedness.

22. (currently amended) The method of claim 1, further including:

transmitting over a computer network the physical location of a patient from which the ~~microorganism bacterium~~ sample is taken;

storing the physical location in the database; and

determining a path of transmission of ~~an infection~~ the bacteria based on the phylogenetic relatedness determination and the physical location of the patient.

23. (previously amended) The method of claim 22, further including:

storing a map of the physical location in the database; and

determining the spread of the infection based on the map of the physical location.

24. (previously amended) The method of claim 23, further including:

sensing the patient's physical location prior to transmitting the patient's physical location.

25. (currently amended) The method of claim 1, further including:

determining the virulence of the ~~microorganism~~ bacterium by retrieving the virulence data of identical or similar ~~microorganisms~~ bacteria from the database; and  
transmitting over a computer network virulence information to a location where the ~~microorganism~~ bacterium sample was obtained.

26. (currently amended) The method of claim 1, ~~wherein the step of providing infection control information comprises:~~ further comprising:

determining drug resistance and treatment information of the ~~microorganism~~ bacterium by retrieving drug information data of identical or similar ~~microorganisms~~ bacteria from the database; and

transmitting over a computer network the drug information data to a location where the ~~microorganism~~ bacterium sample was obtained.

27. (currently amended) The method of claim 1, further including:

determining whether a location where the ~~microorganism~~ bacterium sample was obtained has an outbreak problem; and  
transmitting over a computer network an outbreak warning to the location where the ~~microorganism~~ bacterium sample was obtained.

28. (currently amended) The method of claim 1, further including:

sequencing a second region of the nucleic acid of the ~~microorganism~~ bacterium sample;

and

comparing the second sequenced region with corresponding historical sequence data

derived from known bacteria of the same species and stored in the database;

determining a measure of phylogenetic relatedness between the ~~microorganism sample~~

second region and the corresponding historical sequence data stored in the database based on the comparison of the second sequenced region.

29. (original) The method of claim 28, wherein the determination of relatedness based on the second sequenced region is used to verify the determination of relatedness based on the first sequenced region.

30. (currently amended) The method of claim 28, further including:

identifying a first level of subspecies of the ~~microorganism~~ bacterium sample based on the first sequenced region; and

identifying a second level of subspecies of the ~~microorganism~~ bacterium sample based on the second sequenced region.

31. (original) The method of claim 28, further including:

tracking the global spread of an infection based on sequencing and comparing a slowly mutating region of the nucleic acid; and

tracking the local spread of an infection based on sequencing and comparing a more rapidly mutating region of the nucleic acid.

32. (currently amended) A system for performing real-time infection control over a computer network tracking spread of infectious bacteria, comprising:

- a computer network;
- a centralized database;
- a remote facility connected to the computer network, the remote facility obtaining a sample of a microorganism bacterium;
- a server connected to the computer network, the server receiving sequence data for a first sequenced region of a nucleic acid from the microorganism bacterium sample,
- accessing the centralized database and comparing the first sequenced region with historical sequence data derived from know bacteria of the same species and stored in the centralized database,
- determining a measure of phylogenetic relatedness between the microorganism sample first sequenced region and the historical samples stored in the centralized database, and the historical sequence data
- transmitting infection control information identifying patients infected or objects contaminated with the bacterium based on the phylogenetic relatedness determination to the remote facility over the computer network, thereby allowing the remote facility to use the infection control information to control or prevent the spread of an infection, and transmitting infection and contamination identification over the computer network to the remote facility, thereby allowing the remote facility to track spread of the bacteria.

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33. (currently amended) Computer executable software code stored on a computer

readable medium, performing a method of real time infection control tracking spread of infectious bacteria over a computer network, comprising:

obtaining a sample of a microorganism bacterium;

sequencing a first region of a nucleic acid from the microorganism bacterium sample;

comparing the first sequenced region with historical sequence data derived from known bacteria of the same species stored in a centralized database;

determining a measure of phylogenetic relatedness between the microorganism sample first region and historical sequence data; samples stored in the centralized database; and providing infection control bacterial spread information based on the phylogenetic relatedness determination, thereby allowing use of the infection control bacterial spread information to control or prevent the track spread of an infection.

34. (previously added) The method of claim 1, wherein the sample is obtained at a facility remote from where the sequencing is carried out.

35. (currently amended) The method of claim 34, wherein the remote facility is a health care facility, and a the sample of a microorganism the bacterium is obtained from a prospective patient before as the patient is admitted to a health care facility and prior to being exposed to patients in a the health care facility.

36. (previously added) The method of claim 1, wherein the sample is obtained at a facility remote from where the sequencing, comparing and determination of a measure of phylogenetic relatedness are carried out.

37. canceled

38. (new) The method according to claim 1, wherein infected patients are identified prior to an outbreak of the bacterial infection.

39. (new) A method of tracking spread of infections microorganisms, comprising:  
obtaining a sample of a microorganism;  
sequencing a first region of deoxyribonucleic acid from the microorganism sample, the first region comprising a plurality of repeating sequences of nucleotides;  
comparing the first sequenced region with historical sequence data derived from known microorganisms of the same species stored in a database;  
determining a measure of phylogenetic relatedness between the first sequenced region and the historical sequence data stored in the database based upon differences between the first sequenced region and the historical sequence data;  
identifying patients infected or objects contaminated with the microorganism based on the phylogenetic relatedness determination; and  
tracking the spread of the bacteria utilizing the identified patients and objects.

40. (new) A method of tracking spread of infectious bacteria, viruses and fungi, comprising:

obtaining a sample of a bacterium, virus or fungus;  
sequencing a first region of deoxyribonucleic acid from the sample;

comparing the first sequenced region with historical sequence data derived from known bacteria, viruses or fungi of the same species stored in a database;

determining a measure of phylogenetic relatedness between the first sequenced region and the historical sequence data stored in the database based upon differences between the first sequenced region and the historical sequence data;

identifying patients infected or objects contaminated with the bacterium, virus or fungus based on the phylogenetic relatedness determination; and

tracking the spread of the microorganisms utilizing the identified infected patients and contaminated objects.

41. (new) The method according to claim 1, wherein a plurality of regions of nucleic acid from the sample are sequenced and compared to historical sequence data and the measure of the phylogenetic relatedness between the plurality of sequenced regions and the historical sequence data is determined.

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